STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 148592

TO: Vanessa L Ford **Location: 3b25 / 3c18** **Monday, March 28, 2005** **Art Unit: 1645** **Phone: 571-272-0857** **Serial Number: 10 / 017168**	**From: Jan Delaval** **Location: Biotech-Chem Library** **Remsen 1a51** **Phone: 571-272-22504** **jan.delaval@uspto.gov**

Search Notes

From: Chan, Christina
Sent: Wednesday, March 23, 2005 8:02 AM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017,168 Sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Ford, Vanessa
Sent: Tuesday, March 22, 2005 7:04 PM
To: Chan, Christina
Subject: In re: 10/017,168 Sequence search

Please search SEQ ID NOs: 1, 3,5,19, 21, 23 and 25. Please include interference searches. Please rush.
Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
Art unit:1645

****
STAFF USE ONLY
Searcher:
Searcher Phone: 2-2504
Date Searcher Picked up: 3/23/05
Date Completed: 3/24/05
Searcher Prep/Rev. Time: 20
Online Time: 25

****
Type of Search
NA#: C AA#:
Interference: SPDI:
S/L: Oligomer:
Encode/Transl:
Structure#: Text:
Inventor: Litigation:

****
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other(Specify):

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 1661.36 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-1
Perfect score: 2945
Sequence: 1 gtcgatgcacagctgacgct.....ccgcgttgaacgtcacagtc 2945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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3		856.8	29.1	939	4	AAC84649	Aac84649 T. pallid
4		621.6	21.1	699	4	AAC84648	Aac84648 T. pallid
c	5	284	9.6	486	2	AAX88417	Aax88417 JP1119208
c	6	281.4	9.6	408	2	AAV65195	Aav65195 T. pallid
c	7	281.4	9.6	416	2	AAV53665	Aav53665 Coding se
c	8	281.4	9.6	801	3	AAZ99248	Aaz99248 Nucleotid
c	9	278.4	9.5	468	2	AAV53671	Aav53671 Wild type
c	10	278.4	9.5	468	10	ADK65584	Adk65584 Treponema
c	11	278.2	9.4	492	3	AAA90302	Aaa90302 Modified
c	12	276.8	9.4	468	10	ADC51578	Adc51578 DNA encod
c	13	261.8	8.9	1664	2	AAV53667	Aav53667 Coding se
	14	204.8	7.0	1926	10	ADK65580	Adk65580 Human her
	15	204.6	6.9	1926	3	AAA50254	Aaa50254 Epstein B
	16	204.6	6.9	1926	4	AAF82902	Aaf82902 EBV tethe
	17	204.6	6.9	2580	3	AAA75454	Aaa75454 Nucleotid
	18	204.6	6.9	2580	6	AAI64275	Aai64275 Epstein-B
c	19	204.6	6.9	5452	2	AAX90923	Aax90923 Anti-sens
c	20	204.6	6.9	8705	2	AAZ23778	Aaz23778 Vector pS
c	21	204.6	6.9	8705	12	ADM10659	Adm10659 Expressio
c	22	204.6	6.9	9482	12	ADP64415	Adp64415 Vector pC
	23	204.6	6.9	9600	2	AAV21683	Aav21683 Vector pl
c	24	204.6	6.9	10285	6	ABS71027	Abs71027 pCEP-Xa-F
c	25	204.6	6.9	10285	6	ABS66453	Abs66453 Plasmid p
c	26	204.6	6.9	10330	12	ADL67154	Adl67154 Plasmid p
	27	204.6	6.9	10380	2	AAZ22248	Aaz22248 Nucleotid
c	28	204.6	6.9	10477	12	ADL67152	Adl67152 Plasmid p
c	29	204.6	6.9	10516	12	ADL67150	Adl67150 Plasmid p
c	30	204.6	6.9	10561	12	ADL67148	Adl67148 Plasmid p
	31	204.6	6.9	10596	2	AAQ51731	Aaq51731 Plasmid p
	32	204.6	6.9	10596	2	AAX15650	Aax15650 Nucleotid
	33	204.6	6.9	10596	2	AAT40348	Aat40348 Plasmid p
c	34	204.6	6.9	10615	12	ADL67175	Adl67175 Plasmid p
c	35	204.6	6.9	10774	12	ADL67153	Adl67153 Plasmid p
c	36	204.6	6.9	10921	12	ADL67151	Adl67151 Plasmid p
c	37	204.6	6.9	10961	12	ADL67149	Adl67149 Plasmid p
c	38	204.6	6.9	11006	12	ADL67147	Adl67147 Plasmid p
c	39	204.6	6.9	11059	12	ADL67176	Adl67176 Plasmid p
c	40	204.6	6.9	11693	13	ADR12379	Adr12379 Vector pC
	41	204.6	6.9	11924	12	ADO07395	Ado07395 Modified
	42	204.6	6.9	12242	12	ADO07394	Ado07394 Modified
c	43	204.6	6.9	16080	3	AAA59553	Aaa59553 DNA clone
c	44	204.6	6.9	17753	12	ADL71910	Adl71910 Expressio
	45	204.6	6.9	172281	12	ADN12161	Adn12161 Epstein-B

ALIGNMENTS

RESULT 1
AAC84647
ID AAC84647 standard; DNA; 2945 BP.
XX
AC AAC84647;
XX
DT 11-SEP-2003 (revised)
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein (arp) encoding DNA.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel; ds.
XX
OS Treponema pallidum; ssp. pallidum.
XX
FH Key Location/Qualifiers
FT CDS 919. .2217
FT /*tag= a
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
DR P-PSDB; AAB48316.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 19; Fig 5; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:14 ; Search time 10458.6 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-1
Perfect score: 2945
Sequence: 1 gtcgatgcacagctgacgct.....ccgcgttgaacgtcacagtc 2945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	203.2	6.9	1484	9	CL079800	CL079800 CH216-156
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	3	199.8	6.8	1314	9	CG748456	CG748456 P042-2-D1
c	4	199.6	6.8	1204	8	CC284084	CC284084 CH261-167
	5	199.2	6.8	1047	6	CB905697	CB905697 tric075xl
	6	199.2	6.8	1047	7	CF877361	CF877361 tric075xl
	7	199.2	6.8	1178	9	CG751365	CG751365 P045-4-D0
c	8	199	6.8	1170	8	CC291804	CC291804 CH261-61G
c	9	199	6.8	1200	8	CC187380	CC187380 CH261-33E
	10	198.6	6.7	1066	6	CB905393	CB905393 tric074xd
	11	198.6	6.7	1066	7	CF876920	CF876920 tric074xd
	12	198.4	6.7	1297	9	CG744520	CG744520 P037-1-E1
c	13	198	6.7	1309	9	CL080508	CL080508 CH216-158
c	14	197.8	6.7	1292	8	CC208790	CC208790 CH261-26P
	15	197.6	6.7	911	9	CR116264	CR116264 Forward s
	16	197.4	6.7	1874	9	AG448338	AG448338 Mus muscu
	17	197.2	6.7	1448	8	CC220110	CC220110 CH261-92F
	18	197	6.7	1068	9	AG429516	AG429516 Mus muscu
c	19	197	6.7	1351	8	CC312666	CC312666 TAM32-32D
c	20	197	6.7	1471	9	CG748176	CG748176 P042-1-A0
c	21	196.8	6.7	1156	8	CC319460	CC319460 TAM32-17H
c	22	196.6	6.7	845	9	CC578225	CC578225 CH240_457
	23	196.6	6.7	1223	9	AG441637	AG441637 Mus muscu
	24	196.4	6.7	1107	6	CB905729	CB905729 tric075xn
	25	196.4	6.7	1107	7	CF877385	CF877385 tric075xn
	26	196.4	6.7	1225	6	CD501543	CD501543 CDA51-D09
	27	196	6.7	994	6	CB907117	CB907117 tric081xg
	28	196	6.7	994	7	CF880301	CF880301 tric081xg
	29	196	6.7	1093	6	CB905750	CB905750 tric075xp
	30	196	6.7	1093	7	CF877401	CF877401 tric075xp
c	31	196	6.7	1647	9	AG361024	AG361024 Mus muscu
c	32	195.6	6.6	1288	8	CC220182	CC220182 CH261-23J
c	33	195.6	6.6	1788	8	CC320563	CC320563 TAM32-34P
c	34	195.4	6.6	1214	9	AG324452	AG324452 Mus muscu
c	35	195.4	6.6	1252	9	CG752943	CG752943 P047-4-D1
	36	195.4	6.6	1318	7	CF874345	CF874345 tric006xn
	37	195.4	6.6	1601	9	CG752479	CG752479 P047-2-A0
	38	195.2	6.6	1117	6	CB905666	CB905666 tric075xj
	39	195.2	6.6	1117	7	CF877340	CF877340 tric075xj
	40	194.6	6.6	997	6	CB905724	CB905724 tric075xn
	41	194.6	6.6	997	7	CF877382	CF877382 tric075xn
c	42	194.6	6.6	1217	8	CC222933	CC222933 CH261-40G
c	43	194.6	6.6	1397	9	CL105166	CL105166 ISB1-44E1
	44	194.4	6.6	1011	6	CB905602	CB905602 tric075xf
	45	194.4	6.6	1011	7	CF877292	CF877292 tric075xf

ALIGNMENTS

RESULT 1
CL079800/c
LOCUS CL079800 1484 bp DNA linear GSS 31-DEC-2003
DEFINITION CH216-156O23_Sp5.1 CH216 Xenopus tropicalis genomic clone CH216-156O23, genomic survey sequence.
ACCESSION CL079800
VERSION CL079800.1 GI:40535713
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1484)
AUTHORS Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
High quality sequence start: 549
High quality sequence stop: 627.
FEATURES Location/Qualifiers
source 1. .1484
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-156O23"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"
ORIGIN

Query Match 6.9%; Score 203.2; DB 9; Length 1484;
Best Local Similarity 51.4%; Pred. No. 4.9e-44;
Matches 436; Conservative 0; Mismatches 413; Indels 0; Gaps 0;

Qy 1298 GTGAGGTGGAGGACGCGCCGAAGGTAGTGGAGCCGGCCTCTGAGCGTGAGGGAGGGGAGC 1357

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 13156.4 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-1
Perfect score: 2945
Sequence: 1 gtcgatgcacagctgacgct.....ccgcgttgaacgtcacagtc 2945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2945	100.0	2945	6	AX068032	AX068032 Sequence
	2	2934	99.6	2946	1	AF015824	AF015824 Treponema
	3	1766.6	60.0	14268	1	AE001220	AE001220 Treponema
	4	1634.4	55.5	1647	1	AF411124	AF411124 Treponema
	5	896.4	30.4	1287	1	AF342807	AF342807 Treponema
	6	856.8	29.1	939	6	AX068036	AX068036 Sequence
	7	777	26.4	1182	1	AF411126	AF411126 Treponema
	8	642	21.8	1047	1	AF342806	AF342806 Treponema
	9	621.6	21.1	699	6	AX068034	AX068034 Sequence
	10	361	12.3	14369	1	AE001221	AE001221 Treponema
c	11	351	11.9	660	1	TRP17LPOPR	M74825 Treponema p
c	12	284	9.6	486	6	E27362	E27362 Treponema p
c	13	281.4	9.6	408	6	AX002218	AX002218 Sequence
c	14	281.4	9.6	416	6	E16806	E16806 DNA encodin
c	15	278.4	9.5	468	6	E16811	E16811 DNA encodin
c	16	278.4	9.5	468	6	E16827	E16827 DNA encodin
c	17	261.8	8.9	1664	6	E16823	E16823 DNA encodin
	18	247	8.4	197411	10	AC135961	AC135961 Mus muscu
	19	244	8.3	211580	2	AC111089	AC111089 Mus muscu
c	20	242.6	8.2	178757	10	AC122509	AC122509 Mus muscu
	21	234.6	8.0	205054	10	AC098712	AC098712 Mus muscu
c	22	233.4	7.9	144093	10	AC109193	AC109193 Mus muscu
	23	231.8	7.9	124244	10	AL929026	AL929026 Mouse DNA
	24	231.8	7.9	178620	10	AC121865	AC121865 Mus muscu
c	25	231.8	7.9	179206	2	AC124108	AC124108 Mus muscu
c	26	230.4	7.8	200574	10	BX005304	BX005304 Mouse DNA
	27	230.2	7.8	165592	10	AC122020	AC122020 Mus muscu
c	28	230.2	7.8	194387	10	AC105989	AC105989 Mus muscu
	29	229.4	7.8	110000	2	AC120236_0	AC120236 Rattus no
	30	229.4	7.8	152618	10	AC127583	AC127583 Mus muscu
c	31	228.6	7.8	194736	10	AC126271	AC126271 Mus muscu
c	32	226.8	7.7	120487	10	AC103637	AC103637 Mus muscu
	33	226.6	7.7	152435	10	AC121566	AC121566 Mus muscu
c	34	225.4	7.7	199378	2	AC108256	AC108256 Rattus no
c	35	225.2	7.6	171593	10	AC122052	AC122052 Mus muscu
c	36	224.2	7.6	237814	10	AC091464	AC091464 Mus muscu
c	37	223.2	7.6	157754	10	AC132313	AC132313 Mus muscu
	38	222.2	7.5	195690	10	AC098726	AC098726 Mus muscu
	39	222	7.5	240931	2	AC107097	AC107097 Rattus no
	40	221.6	7.5	76941	10	BX000698	BX000698 Mouse DNA
c	41	221.4	7.5	187287	10	AL928735	AL928735 Mouse DNA
	42	220.2	7.5	187126	10	AC113315	AC113315 Mus muscu
	43	219.8	7.5	97839	2	AC141520	AC141520 Rattus no
	44	219.8	7.5	215745	10	AC117585	AC117585 Mus muscu
c	45	219.8	7.5	234888	2	AC102097	AC102097 Mus muscu

ALIGNMENTS

RESULT 1
AX068032
LOCUS AX068032 2945 bp DNA linear PAT 21-JAN-2001
DEFINITION Sequence 1 from Patent WO0077486.
ACCESSION AX068032
VERSION AX068032.1 GI:12329840
KEYWORDS .
SOURCE Treponema pallidum
ORGANISM Treponema pallidum
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE 1
AUTHORS Liu,H., Steiner,B. and Rhodes,B.
TITLE Compositions and methods for detecting Treponema pallidum
JOURNAL Patent: WO 0077486-A 1 21-DEC-2000;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES Location/Qualifiers
source 1. .2945
/organism="Treponema pallidum"
/mol_type="unassigned DNA"
/db_xref="taxon:160"
CDS 919. .2217
/note="unnamed protein product; Subspecies: pallidum (Nichols strain)"
/codon_start=1
/transl_table=11
/protein_id="CAC24646.1"
/db_xref="GI:12329841"
/translation="MFVRSDMFPKNTAVEISNLEKNAKAQAVVIGHAGIPGLLVSLAP
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EREGGEREVEDVPKVVEPASEREGGEREVEDAPKVVEPASEREGGEREVEDVPKVVEP
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EPASEREGGEREVEDVPKVVEPASEREGGEREVEDVPKVVEPASEREGGEREVEDVPK
VVEPASEREGGEREVEDVPKVVEPASEREGGEREVEDVPGVVEPASGHEGGEREVEDV
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ORIGIN

Query Match 100.0%; Score 2945; DB 6; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGATGCACAGCTGACGCTCTCAGGTCTTGCACATATTGCGCGGCTGGTGCCGACATCT 60

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 394.326 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-3
Perfect score: 699
Sequence: 1 atgtttgtgcgcagtgacat.....atcagtttcggaaaccctga 699

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	699	100.0	699	4	AAC84648	Aac84648 T. pallid
	2	626.4	89.6	939	4	AAC84649	Aac84649 T. pallid
	3	621.6	88.9	2945	4	AAC84647	Aac84647 T. pallid
	4	537.8	76.9	9410	2	AAX20603	Aax20603 Polynucle
	5	82.6	11.8	149158	12	ADP74211	Adp74211 Equine he
c	6	82.6	11.8	149158	12	ADP74211	Adp74211 Equine he
	7	82.6	11.8	149261	12	ADP74212	Adp74212 Equine he
c	8	82.6	11.8	149261	12	ADP74212	Adp74212 Equine he
	9	82.6	11.8	150071	12	ADP74216	Adp74216 Equine he
c	10	82.6	11.8	150071	12	ADP74216	Adp74216 Equine he
	11	82.6	11.8	150223	12	ADP74201	Adp74201 Equine he
c	12	82.6	11.8	150223	12	ADP74201	Adp74201 Equine he
c	13	80.6	11.5	110000	8	ABX16390_2	Continuation (3 of
	14	78.2	11.2	628	12	ACH89664	Ach89664 Human gen
	15	77.6	11.1	3127	12	ADN12154	Adn12154 Kaposis s
c	16	77.4	11.1	114793	4	AAD08215	Aad08215 Human gen
	17	77.2	11.0	3012	12	ADN12155	Adn12155 Herpesvir
c	18	75.8	10.8	7720	3	AAA53800	Aaa53800 Genomic D
	19	75.8	10.8	8298	4	AAK72613	Aak72613 Human imm
c	20	75	10.7	16442	2	AAX83006	Aax83006 Partial m
	21	73.4	10.5	795	2	AAV55830	Aav55830 FLGA inse
	22	73.4	10.5	799	2	AAV55831	Aav55831 Nucleotid
	23	73.4	10.5	1925	2	AAX90924	Aax90924 Epstein B
	24	73.4	10.5	1926	3	AAA50254	Aaa50254 Epstein B
	25	73.4	10.5	1926	4	AAF82902	Aaf82902 EBV tethe
	26	73.4	10.5	1926	10	ADK65580	Adk65580 Human her
	27	73.4	10.5	2580	3	AAA75454	Aaa75454 Nucleotid
	28	73.4	10.5	2580	6	AAI64275	Aai64275 Epstein-B
c	29	73.4	10.5	5452	2	AAX90923	Aax90923 Anti-sens
c	30	73.4	10.5	8705	2	AAZ23778	Aaz23778 Vector pS
c	31	73.4	10.5	8705	12	ADM10659	Adm10659 Expressio
c	32	73.4	10.5	9482	12	ADP64415	Adp64415 Vector pC
	33	73.4	10.5	9600	2	AAV21683	Aav21683 Vector pl
c	34	73.4	10.5	10285	6	ABS71027	Abs71027 pCEP-Xa-F
c	35	73.4	10.5	10285	6	ABS66453	Abs66453 Plasmid p
c	36	73.4	10.5	10330	12	ADL67154	Adl67154 Plasmid p
	37	73.4	10.5	10380	2	AAZ22248	Aaz22248 Nucleotid
c	38	73.4	10.5	10477	12	ADL67152	Adl67152 Plasmid p
c	39	73.4	10.5	10516	12	ADL67150	Adl67150 Plasmid p
c	40	73.4	10.5	10561	12	ADL67148	Adl67148 Plasmid p
	41	73.4	10.5	10596	2	AAQ51731	Aaq51731 Plasmid p
	42	73.4	10.5	10596	2	AAX15650	Aax15650 Nucleotid
	43	73.4	10.5	10596	2	AAT40348	Aat40348 Plasmid p
c	44	73.4	10.5	10615	12	ADL67175	Adl67175 Plasmid p
c	45	73.4	10.5	10774	12	ADL67153	Adl67153 Plasmid p

ALIGNMENTS

RESULT 1
AAC84648
ID AAC84648 standard; DNA; 699 BP.
XX
AC AAC84648;
XX
DT 11-SEP-2003 (revised)
DT 20-APR-2001 (first entry)
XX
DE T. pallidum (CDC-2) acidic repeat protein (arp) encoding DNA.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel; ds.
XX
OS Treponema pallidum; ssp. pertenue.
XX
FH Key Location/Qualifiers
FT CDS 1. .699
FT /*tag= a
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
DR P-PSDB; AAB48317.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 19; Fig 7; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:14 ; Search time 2482.36 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-3
Perfect score: 699
Sequence: 1 atgtttgtgcgcagtgacat.....atcagtttcggaaaccctga 699

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	89.6	12.8	365	9	L2644X	AL160994 Leishmani
c 2	85.8	12.3	293	8	AZ334000	AZ334000 1M0063P17
c 3	83	11.9	776	9	AG561854	Mus muscu
c 4	81.4	11.6	709	9	AG351718	AG351718 Mus muscu
c 5	77	11.0	697	6	BY752869	BY752869 BY752869
c 6	76.6	11.0	514	8	BZ089457	CH230-1C1
c 7	76.6	11.0	783	9	AG573654	AG573654 Mus muscu
c 8	75.4	10.8	820	9	CL836578	CL836578 OR_CBa006
9	73.4	10.5	482	7	CV254879	WS02411.B
10	73.2	10.5	752	9	AG562801	AG562801 Mus muscu
c 11	72.8	10.4	650	8	AZ337339	AZ337339 1M0068B03
12	72.2	10.3	384	9	CNS01145	AL099791 Drosophil
13	71.8	10.3	523	8	AZ383375	AZ383375 1M0141E03
c 14	71.8	10.3	979	6	CD328191	CD328191 AGENCOURT
15	71.4	10.2	419	4	BG273097	nai99f06.
c 16	70.8	10.1	1945	8	CC251395	CC251395 CH261-157
c 17	70.6	10.1	275	7	CO546011	CO546011 LyEST2038
c 18	70.4	10.1	733	9	CC641774	OGUBU35TH
c 19	70.4	10.1	852	8	BZ801844	BZ801844 PUGAG07TB
c 20	70.4	10.1	945	9	CG344918	CG344918 OG2BH42TH
c 21	70.4	10.1	1099	9	CL509275	CL509275 SAIL_811_
22	70.2	10.0	617	9	CE019059	CE019059 tigr-gss-
23	70.2	10.0	696	7	CK138139	CK138139 VRJ135 Vi
c 24	70	10.0	834	9	AG555306	AG555306 Mus muscu
c 25	70	10.0	1197	9	AG346705	AG346705 Mus muscu
c 26	69.4	9.9	427	7	CK286024	CK286024 EST748746
c 27	69.4	9.9	1147	8	BZ051981	BZ051981 jnr56f09.
28	69.2	9.9	699	6	CD493768	CD493768 CDA07-A05
c 29	69.2	9.9	1271	9	CL492192	CL492192 SAIL_564_
30	69	9.9	430	5	BM900946	BM900946 rc43c10.y
31	69	9.9	986	9	AG390365	AG390365 Mus muscu
c 32	68.6	9.8	494	7	CF609053	CF609053 GERMO01_0
c 33	68.6	9.8	516	7	CF607575	CF607575 GEMMA01_0
34	68.6	9.8	583	5	BQ847872	BQ847872 QGA5J16.y
c 35	68.6	9.8	1344	9	AG435591	AG435591 Mus muscu
c 36	68.4	9.8	501	7	CV094178	CV094178 FAMU_USDA
c 37	68.4	9.8	520	7	CV096855	CV096855 FAMU_USDA
c 38	68.4	9.8	552	7	CN605345	CN605345 USDA_FP_1
c 39	68.4	9.8	592	7	CV092833	CV092833 FAMU_USDA
c 40	68.4	9.8	609	7	CV099895	CV099895 FAMU_USDA
c 41	68.4	9.8	624	7	CV092434	CV092434 FAMU_USDA
c 42	68.4	9.8	647	7	CV096641	CV096641 FAMU_USDA
c 43	68.4	9.8	651	7	CV093263	CV093263 FAMU_USDA
c 44	68.4	9.8	651	7	CV097413	CV097413 FAMU_USDA
c 45	68.4	9.8	688	7	CV098193	CV098193 FAMU_USDA

ALIGNMENTS

RESULT 1
L2644X/c
LOCUS L2644X 365 bp DNA linear GSS 16-MAR-2000
DEFINITION Leishmania major Friedlin cosmid L2644 t3Hyg end-sequence, similar to U40394 U40394 Kaposi's sarcoma-associated herpes-like. . ., N=755, Prob=1.8e-54; TR:P93797 P93797 PHEROPHORIN-S PRECURSOR. [0] +3. . ., N=318, Prob=7.2e-37, genomic survey sequence.
ACCESSION AL160994
VERSION AL160994.1 GI:7258621
KEYWORDS GSS.
SOURCE Leishmania major
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
REFERENCE 1 (bases 1 to 365)
AUTHORS Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.
TITLE A physical map of the Leishmania major Friedlin genome
JOURNAL Genome Res. 8 (2), 135-145 (1998)
MEDLINE 98146435
PUBMED 9477341
REFERENCE 2 (bases 1 to 67)
AUTHORS Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk
COMMENT see http://www.ebi.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/
The cLHYG t3Hyg primer sequence can be obtained from acc. no. U59231.
FEATURES Location/Qualifiers
source 1. .365
/organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/chromosome="26"
/clone="cosmid L2644"
ORIGIN

Query Match 12.8%; Score 89.6; DB 9; Length 365;
Best Local Similarity 58.7%; Pred. No. 4.5e-13;
Matches 155; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 3122.69 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-3
Perfect score: 699
Sequence: 1 atgtttgtgcgcagtgacat.....atcagtttcggaaaccctga 699

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	699	100.0	699	6	AX068034	AX068034 Sequence
	2	693.4	99.2	1047	1	AF342806	AF342806 Treponema
	3	626.4	89.6	939	6	AX068036	AX068036 Sequence
	4	626.4	89.6	1287	1	AF342807	AF342807 Treponema
	5	621.6	88.9	1647	1	AF411124	AF411124 Treponema
	6	621.6	88.9	2945	6	AX068032	AX068032 Sequence
	7	621.6	88.9	2946	1	AF015824	AF015824 Treponema
	8	608.8	87.1	14268	1	AE001220	AE001220 Treponema
	9	601.4	86.0	1182	1	AF411126	AF411126 Treponema
	10	89.4	12.8	211580	2	AC111089	AC111089 Mus muscu
	11	88.4	12.6	165592	10	AC122020	AC122020 Mus muscu
	12	87.8	12.6	219771	2	BX005376	BX005376 Danio rer
	13	87.8	12.6	253504	10	AC102602	AC102602 Mus muscu
	14	87.8	12.6	266556	2	AC136868	AC136868 Rattus no
c	15	87.6	12.5	233939	2	AC105853	AC105853 Rattus no
	16	87.2	12.5	269572	2	AC108552	AC108552 Rattus no
c	17	86.8	12.4	110000	10	AE016753_2	Continuation (3 of
	18	86.8	12.4	152435	10	AC121566	AC121566 Mus muscu
	19	86.2	12.3	125681	10	AC122889	AC122889 Mus muscu
c	20	86.2	12.3	161905	10	AL929034	AL929034 Mouse DNA
c	21	86.2	12.3	178757	10	AC122509	AC122509 Mus muscu
	22	86.2	12.3	196236	10	AC108780	AC108780 Mus muscu
	23	86.2	12.3	197411	10	AC135961	AC135961 Mus muscu
c	24	86.2	12.3	203086	10	AC099948	AC099948 Mus muscu
c	25	86.2	12.3	215769	10	AC100209	AC100209 Mus muscu
	26	85.6	12.2	192371	10	AC123857	AC123857 Mus muscu
	27	85.6	12.2	199459	10	AC125192	AC125192 Mus muscu
	28	85.2	12.2	143913	2	AC124827	AC124827 Mus muscu
c	29	84.6	12.1	120487	10	AC103637	AC103637 Mus muscu
c	30	84.6	12.1	163882	10	AC133904	AC133904 Mus muscu
c	31	84.6	12.1	171593	10	AC122052	AC122052 Mus muscu
	32	84.6	12.1	179063	10	AC145590	AC145590 Mus muscu
c	33	84.6	12.1	191753	10	AC125235	AC125235 Mus muscu
c	34	84.6	12.1	199854	10	AL591208	AL591208 Mouse DNA
c	35	84.6	12.1	210595	2	AC116862	AC116862 Mus muscu
c	36	84.6	12.1	215620	10	AL928551	AL928551 Mouse DNA
c	37	84.6	12.1	217353	10	AC149611	AC149611 Mus muscu
	38	84.6	12.1	229190	10	AC127348	AC127348 Mus muscu
c	39	84.6	12.1	234888	2	AC102097	AC102097 Mus muscu
c	40	84.6	12.1	260625	2	AC096018	AC096018 Rattus no
	41	84.6	12.1	289751	10	AC091458	AC091458 Mus muscu
	42	84	12.0	179886	2	AC140072	AC140072 Mus muscu
c	43	84	12.0	182272	10	AC122232	AC122232 Mus muscu
c	44	84	12.0	208880	10	AC123837	AC123837 Mus muscu
c	45	84	12.0	219568	10	AL844840	AL844840 Mouse DNA

ALIGNMENTS

RESULT 1
AX068034
LOCUS AX068034 699 bp DNA linear PAT 19-JAN-2001
DEFINITION Sequence 3 from Patent WO0077486.
ACCESSION AX068034
VERSION AX068034.1 GI:12329842
KEYWORDS .
SOURCE Treponema pallidum
ORGANISM Treponema pallidum
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE 1
AUTHORS Liu,H., Steiner,B. and Rhodes,B.
TITLE Compositions and methods for detecting Treponema pallidum
JOURNAL Patent: WO 0077486-A 3 21-DEC-2000;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES Location/Qualifiers
source 1. .699
/organism="Treponema pallidum"
/mol_type="unassigned DNA"
/db_xref="taxon:160"
CDS 1. .699
/note="unnamed protein product; Subspecies: pertenue (CDC-2 strain)"
/codon_start=1
/transl_table=11
/protein_id="CAC24647.1"
/db_xref="GI:12329843"
/translation="MFVRSDMFPKNTAVEISNLEKNAKAQAVVIGHAGIPGLLVSLAP AAAAQLGIGVYQAVRVRVRTLGTVRGGSQTSQDGLSLASLPSRVPARPAQRDPLSSPP AGHTVPEYRDTVIFDDPRLVSPLSREVEDVPKVVEPASEREGGEREVEDVPKVVEPAS EREGGEREVEDVPKVVEPASEREGGEREVEDVPKVVEPASEREGGEREVASQHTKQPS HSVSNSAPNQFRKP"
ORIGIN

Query Match 100.0%; Score 699; DB 6; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.5e-145;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTTGTGCGCAGTGACATGTTCCCCAAAAACACTGCTGTTGAAATTAGCAACTTAGAA 60
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Db 1 ATGTTTGTGCGCAGTGACATGTTCCCCAAAAACACTGCTGTTGAAATTAGCAACTTAGAA 60

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 4194.86 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-5
Perfect score: 939
Sequence: 1 atgtttgtgcgcagtgacat.....atcagtttcggaaaccctga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	858.4	91.4	1647	1	AF411124	AF411124 Treponema
	4	856.8	91.2	2945	6	AX068032	AX068032 Sequence
	5	856.8	91.2	2946	1	AF015824	AF015824 Treponema
	6	771.4	82.2	14268	1	AE001220	AE001220 Treponema
	7	721.4	76.8	1182	1	AF411126	AF411126 Treponema
	8	626.4	66.7	699	6	AX068034	AX068034 Sequence
	9	626.4	66.7	1047	1	AF342806	AF342806 Treponema
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c	11	163	17.4	178757	10	AC122509	AC122509 Mus muscu
	12	154.4	16.4	197411	10	AC135961	AC135961 Mus muscu
c	13	152.2	16.2	260625	2	AC096018	AC096018 Rattus no
c	14	150.2	16.0	318930	2	AC073495	AC073495 Mus muscu
c	15	149.6	15.9	216602	10	AC136729	AC136729 Mus muscu
c	16	148.6	15.8	163945	2	AC116727	AC116727 Mus muscu
c	17	148.6	15.8	217353	10	AC149611	AC149611 Mus muscu
	18	148.6	15.8	229190	10	AC127348	AC127348 Mus muscu
	19	148	15.8	165592	10	AC122020	AC122020 Mus muscu
	20	147.8	15.7	211161	2	AC098271	AC098271 Rattus no
	21	147.6	15.7	152618	10	AC127583	AC127583 Mus muscu
	22	145.8	15.5	197683	10	AC118476	AC118476 Mus muscu
c	23	145.4	15.5	200574	10	BX005304	BX005304 Mouse DNA
	24	145.4	15.5	215745	10	AC117585	AC117585 Mus muscu
c	25	145.4	15.5	237814	10	AC091464	AC091464 Mus muscu
c	26	145	15.4	179206	2	AC124108	AC124108 Mus muscu
c	27	144.8	15.4	144093	10	AC109193	AC109193 Mus muscu
	28	144.6	15.4	110000	2	AC120236_0	AC120236 Rattus no
	29	144.6	15.4	192371	10	AC123857	AC123857 Mus muscu
c	30	144.2	15.4	203490	10	AC122851	AC122851 Mus muscu
c	31	144	15.3	120487	10	AC103637	AC103637 Mus muscu
c	32	144	15.3	171593	10	AC122052	AC122052 Mus muscu
c	33	143.8	15.3	182272	10	AC122232	AC122232 Mus muscu
c	34	143.8	15.3	191753	10	AC125235	AC125235 Mus muscu
c	35	143.2	15.3	194736	10	AC126271	AC126271 Mus muscu
	36	143.2	15.3	205054	10	AC098712	AC098712 Mus muscu
c	37	143	15.2	206497	10	AC084389	AC084389 Mus muscu
	38	142.8	15.2	152435	10	AC121566	AC121566 Mus muscu
	39	142.8	15.2	253504	10	AC102602	AC102602 Mus muscu
	40	142.6	15.2	125681	10	AC122889	AC122889 Mus muscu
	41	142.6	15.2	199459	10	AC125192	AC125192 Mus muscu
	42	142.2	15.1	178620	10	AC121865	AC121865 Mus muscu
	43	142.2	15.1	199854	10	AL591208	AL591208 Mouse DNA
c	44	142.2	15.1	208880	10	AC123837	AC123837 Mus muscu
c	45	142.2	15.1	217522	10	AC117639	AC117639 Mus muscu

ALIGNMENTS

RESULT 1
AX068036
LOCUS AX068036 939 bp DNA linear PAT 19-JAN-2001
DEFINITION Sequence 5 from Patent WO0077486.
ACCESSION AX068036
VERSION AX068036.1 GI:12329844
KEYWORDS .
SOURCE Treponema pallidum
ORGANISM Treponema pallidum
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE 1
AUTHORS Liu,H., Steiner,B. and Rhodes,B.
TITLE Compositions and methods for detecting Treponema pallidum
JOURNAL Patent: WO 0077486-A 5 21-DEC-2000;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES Location/Qualifiers
source 1. .939
/organism="Treponema pallidum"
/mol_type="unassigned DNA"
/db_xref="taxon:160"
CDS 1. .939
/note="unnamed protein product; Subspecies: endemicum (Bosnia strain)"
/codon_start=1
/transl_table=11
/protein_id="CAC24648.1"
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EREGGEREVEDVPKVVEPASEREGGEREVEDVPKVVEPASEREGGEREVEDVPKVVEP
ASEREGGEREVEDVPKVVEPASEREGGEREVEDVPKVV
EPASEREGGEREVASQHTKQPSHSVSNSAPNQFRKP"
ORIGIN

Query Match 100.0%; Score 939; DB 6; Length 939;
Best Local Similarity 100.0%; Pred. No. 9.4e-194;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTTGTGCGCAGTGACATGTTCCCCAAAAACACTGCTGTTGAAATTAGCAACTTAGAA 60
Db 1 ATGTTTGTGCGCAGTGACATGTTCCCCAAAAACACTGCTGTTGAAATTAGCAACTTAGAA 60

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 529.717 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-5
Perfect score: 939
Sequence: 1 atgtttgtgcgcagtgacat.....atcagtttcggaaaccctga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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3		637.2	67.9	9410	2	AAX20603	Aax20603 Polynucle
4		626.4	66.7	699	4	AAC84648	Aac84648 T. pallid
5	c	130	13.8	30191	12	ADQ97654	Adq97654 Mouse can
6		129.4	13.8	799	2	AAV55831	Aav55831 Nucleotid
7		129.4	13.8	1926	3	AAA50254	Aaa50254 Epstein B
8		129.4	13.8	1926	4	AAF82902	Aaf82902 EBV tethe
9		129.4	13.8	1926	10	ADK65580	Adk65580 Human her
10		129.4	13.8	2580	3	AAA75454	Aaa75454 Nucleotid
11		129.4	13.8	2580	6	AAI64275	Aai64275 Epstein-B
12	c	129.4	13.8	5452	2	AAX90923	Aax90923 Anti-sens
13	c	129.4	13.8	8705	2	AAZ23778	Aaz23778 Vector pS
14	c	129.4	13.8	8705	12	ADM10659	Adm10659 Expressio
15	c	129.4	13.8	9482	12	ADP64415	Adp64415 Vector pC
16		129.4	13.8	9600	2	AAV21683	Aav21683 Vector pl
17	c	129.4	13.8	10285	6	ABS71027	Abs71027 pCEP-Xa-F
18	c	129.4	13.8	10285	6	ABS66453	Abs66453 Plasmid p
19	c	129.4	13.8	10330	12	ADL67154	Adl67154 Plasmid p
20		129.4	13.8	10380	2	AAZ22248	Aaz22248 Nucleotid
21	c	129.4	13.8	10477	12	ADL67152	Adl67152 Plasmid p
22	c	129.4	13.8	10516	12	ADL67150	Adl67150 Plasmid p
23	c	129.4	13.8	10561	12	ADL67148	Adl67148 Plasmid p
24		129.4	13.8	10596	2	AAQ51731	Aaq51731 Plasmid p
25		129.4	13.8	10596	2	AAX15650	Aax15650 Nucleotid
26		129.4	13.8	10596	2	AAT40348	Aat40348 Plasmid p
27	c	129.4	13.8	10615	12	ADL67175	Adl67175 Plasmid p
28	c	129.4	13.8	10774	12	ADL67153	Adl67153 Plasmid p
29	c	129.4	13.8	10921	12	ADL67151	Adl67151 Plasmid p
30	c	129.4	13.8	10961	12	ADL67149	Adl67149 Plasmid p
31	c	129.4	13.8	11006	12	ADL67147	Adl67147 Plasmid p
32	c	129.4	13.8	11059	12	ADL67176	Adl67176 Plasmid p
33	c	129.4	13.8	11693	13	ADR12379	Adr12379 Vector pC
34		129.4	13.8	11924	12	ADO07395	Ado07395 Modified
35		129.4	13.8	12242	12	ADO07394	Ado07394 Modified
36	c	129.4	13.8	16080	3	AAA59553	Aaa59553 DNA clone
37	c	129.4	13.8	17753	12	ADL71910	Adl71910 Expressio
38		129.4	13.8	172281	12	ADN12161	Adn12161 Epstein-B
39		129.2	13.8	1925	2	AAX90924	Aax90924 Epstein B
40		128.4	13.7	795	2	AAV55830	Aav55830 FLGA inse
41		125.2	13.3	628	12	ACH89664	Ach89664 Human gen
42	c	120.8	12.9	26214	12	ADQ97246	Adq97246 Mouse can
43		118.8	12.7	12733	6	ABK98631	Abk98631 Vector pE
44		118.8	12.7	12733	9	ACD13882	Acd13882 L. lactis
45		118.8	12.7	12739	6	ABK98592	Abk98592 Vector pE

ALIGNMENTS

RESULT 1
AAC84649
ID AAC84649 standard; DNA; 939 BP.
XX
AC AAC84649;
XX
DT 11-SEP-2003 (revised)
DT 20-APR-2001 (first entry)
XX
DE T. pallidum (Bosnia) acidic repeat protein (arp) encoding DNA.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel; ds.
XX
OS Treponema pallidum; ssp. endemicum.
XX
FH Key Location/Qualifiers
FT CDS 1. .939
FT /*tag= a
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
DR P-PSDB; AAB48318.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 19; Fig 9; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:14 ; Search time 3334.67 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-5
Perfect score: 939
Sequence: 1 atgtttgtgcgcagtgacat.....atcagtttcggaaaccctga 939

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	134.8	14.4	776	9	AG561854	AG561854 Mus muscu
c	2	129	13.7	709	9	AG351718	AG351718 Mus muscu
c	3	126.2	13.4	650	8	AZ337339	AZ337339 1M0068B03
c	4	124.6	13.3	1089	4	BM468944	BM468944 AGENCOURT
	5	122.8	13.1	623	9	CR055317	CR055317 Reverse s
	6	122.8	13.1	1110	9	CL079755	CL079755 CH216-156
	7	122.8	13.1	1313	7	CF874294	CF874294 tric006xm
	8	122.6	13.1	523	8	AZ383375	AZ383375 1M0141E03
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	10	121.2	12.9	1083	7	CV520573	CV520573 0089P0047
	11	121.2	12.9	1448	8	CC220110	CC220110 CH261-92F
	12	120.4	12.8	860	6	CB904993	CB904993 tric040xp
c	13	120.2	12.8	697	6	BY752869	BY752869 BY752869
c	14	120.2	12.8	1031	9	CL492176	CL492176 SAIL_564_
c	15	120.2	12.8	1231	9	AG363910	AG363910 Mus muscu
	16	120	12.8	1555	9	CL073978	CL073978 CH216-131
	17	119.8	12.8	1560	9	CL081488	CL081488 CH216-162
c	18	119.8	12.8	1656	9	AG430456	AG430456 Mus muscu
	19	119.6	12.7	602	9	CR023579	CR023579 Reverse s
c	20	119.6	12.7	870	2	BE258873	BE258873 601116824
c	21	119.6	12.7	1292	8	CC208790	CC208790 CH261-26P
c	22	119.6	12.7	1484	9	CL079800	CL079800 CH216-156
	23	119.2	12.7	817	8	AZ196702	AZ196702 SP_1032_B
	24	119.2	12.7	1546	9	AG435295	AG435295 Mus muscu
	25	119	12.7	935	4	BI958090	BI958090 HVSMEn001
c	26	119	12.7	1153	8	CC294165	CC294165 CH261-130
c	27	118.8	12.7	517	9	TA21B11Q	AL453768 T. brucei
c	28	118.8	12.7	1100	8	CC262597	CC262597 CH261-167
	29	118.8	12.7	1233	9	AG396109	AG396109 Mus muscu
c	30	118.6	12.6	1196	8	CC298943	CC298943 CH261-22C
c	31	118.4	12.6	1035	9	CL086207	CL086207 ISB1-7A17
	32	118.4	12.6	1082	8	CC300639	CC300639 CH261-68J
c	33	118.4	12.6	1309	9	CL080508	CL080508 CH216-158
c	34	118.4	12.6	1373	9	AG435617	AG435617 Mus muscu
c	35	118.2	12.6	548	9	BX121682	BX121682 Danio rer
	36	118.2	12.6	837	9	CR074624	CR074624 Forward s
	37	118.2	12.6	883	8	AZ186646	AZ186646 SP_1007_B
	38	118.2	12.6	911	9	CR116264	CR116264 Forward s
	39	118.2	12.6	1238	9	AG448606	AG448606 Mus muscu
c	40	118.2	12.6	1471	9	CG748176	CG748176 P042-1-A0
	41	118.2	12.6	1696	9	AG382169	AG382169 Mus muscu
c	42	118	12.6	845	9	CC578225	CC578225 CH240_457
	43	118	12.6	1011	6	CB905602	CB905602 tric075xf
	44	118	12.6	1011	7	CF877292	CF877292 tric075xf
	45	118	12.6	1193	9	AG349830	AG349830 Mus muscu

ALIGNMENTS

RESULT 1
AG561854/c
LOCUS AG561854 776 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-481H05.T7, genomic survey sequence.
ACCESSION AG561854
VERSION AG561854.1 GI:48322552
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 776)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .776
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
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/clone="MSMg01-481H05.T7"
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/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 5280.43 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-25
Perfect score: 1182
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1182	100.0	1182	1	AF411126	AF411126 Treponema
	2	1085.2	91.8	14268	1	AE001220	AE001220 Treponema
	3	1067	90.3	1287	1	AF342807	AF342807 Treponema
	4	902	76.3	1047	1	AF342806	AF342806 Treponema
	5	788	66.7	1647	1	AF411124	AF411124 Treponema
	6	777	65.7	2945	6	AX068032	AX068032 Sequence
	7	777	65.7	2946	1	AF015824	AF015824 Treponema
	8	721.4	61.0	939	6	AX068036	AX068036 Sequence
	9	601.4	50.9	699	6	AX068034	AX068034 Sequence
	10	134.8	11.4	211580	2	AC111089	AC111089 Mus muscu
c	11	131.6	11.1	178757	10	AC122509	AC122509 Mus muscu
c	12	130	11.0	215769	10	AC100209	AC100209 Mus muscu
	13	128.6	10.9	266556	2	AC136868	AC136868 Rattus no
	14	128	10.8	199459	10	AC125192	AC125192 Mus muscu
	15	126.8	10.7	125681	10	AC122889	AC122889 Mus muscu
	16	124.2	10.5	165592	10	AC122020	AC122020 Mus muscu
	17	123.6	10.5	253504	10	AC102602	AC102602 Mus muscu
c	18	123	10.4	199854	10	AL591208	AL591208 Mouse DNA
	19	123	10.4	289751	10	AC091458	AC091458 Mus muscu
	20	122.6	10.4	152435	10	AC121566	AC121566 Mus muscu
	21	122.6	10.4	197411	10	AC135961	AC135961 Mus muscu
	22	122.4	10.4	139630	10	AC133945	AC133945 Mus muscu
c	23	122.2	10.3	178258	2	AC109296	AC109296 Mus muscu
c	24	122	10.3	120487	10	AC103637	AC103637 Mus muscu
c	25	122	10.3	171593	10	AC122052	AC122052 Mus muscu
c	26	122	10.3	216602	10	AC136729	AC136729 Mus muscu
c	27	122	10.3	217353	10	AC149611	AC149611 Mus muscu
	28	122	10.3	219771	2	BX005376	BX005376 Danio rer
	29	122	10.3	229190	10	AC127348	AC127348 Mus muscu
c	30	121.6	10.3	260625	2	AC096018	AC096018 Rattus no
c	31	121.4	10.3	182272	10	AC122232	AC122232 Mus muscu
c	32	121.4	10.3	208880	10	AC123837	AC123837 Mus muscu
c	33	121	10.2	163945	2	AC116727	AC116727 Mus muscu
c	34	120.6	10.2	110000	10	AE016753_2	Continuation (3 of
c	35	120.4	10.2	318930	2	AC073495	AC073495 Mus muscu
	36	119.8	10.1	154462	2	AC145149	AC145149 Homo sapi
c	37	119.8	10.1	191753	10	AC125235	AC125235 Mus muscu
	38	119.8	10.1	196236	10	AC108780	AC108780 Mus muscu
	39	119.8	10.1	197683	10	AC118476	AC118476 Mus muscu
c	40	119.8	10.1	203086	10	AC099948	AC099948 Mus muscu
	41	119.8	10.1	215745	10	AC117585	AC117585 Mus muscu
	42	119.6	10.1	211161	2	AC098271	AC098271 Rattus no
c	43	119.2	10.1	172853	10	AC120147	AC120147 Mus muscu
	44	119.2	10.1	182777	10	AC115928	AC115928 Mus muscu
	45	119.2	10.1	192371	10	AC123857	AC123857 Mus muscu

ALIGNMENTS

RESULT 1
AF411126
LOCUS AF411126 1182 bp DNA linear BCT 26-SEP-2001
DEFINITION Treponema pallidum subsp. pertenue strain CDC1 acidic repeat protein (arp) gene, complete cds.
ACCESSION AF411126
VERSION AF411126.1 GI:15778314
KEYWORDS .
SOURCE Treponema pallidum subsp. pertenue (yaws treponeme)
ORGANISM Treponema pallidum subsp. pertenue
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE 1 (bases 1 to 1182)
AUTHORS Liu,H., Steiner,B.M. and Rodes,B.
TITLE Molecular characterization of the acidic repeat protein gene (arp) of Treponema pallidum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1182)
AUTHORS Liu,H., Steiner,B.M. and Rodes,B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) National Center for Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Rd, Atlanta, GA 30333, USA
FEATURES Location/Qualifiers
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/organism="Treponema pallidum subsp. pertenue"
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:14 ; Search time 4197.64 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-25
Perfect score: 1182
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	118.2	10.0	776	9	AG561854	AG561854 Mus muscu
c	2	116.6	9.9	709	9	AG351718	AG351718 Mus muscu
c	3	111.6	9.4	697	6	BY752869	BY752869 BY752869
c	4	107	9.1	650	8	AZ337339	AZ337339 1M0068B03
c	5	103.4	8.7	1945	8	CC251395	CC251395 CH261-157
	6	102.8	8.7	1560	9	CL081488	CL081488 CH216-162
	7	101.8	8.6	1101	9	CNS0181P	AL108775 Drosophil
c	8	101.6	8.6	1231	9	AG363910	AG363910 Mus muscu
	9	101.4	8.6	992	9	CNS04R5Q	AL303479 Tetraodon
	10	101.2	8.6	1110	9	CL079755	CL079755 CH216-156
	11	101.2	8.6	1448	8	CC220110	CC220110 CH261-92F
c	12	101	8.5	870	2	BE258873	BE258873 601116824
	13	101	8.5	1313	7	CF874294	CF874294 tric006xm
c	14	100.8	8.5	1656	9	AG430456	AG430456 Mus muscu
c	15	100.6	8.5	783	9	AG573654	AG573654 Mus muscu
c	16	100	8.5	548	9	BX121682	BX121682 Danio rer
c	17	100	8.5	1100	8	CC262597	CC262597 CH261-167
c	18	100	8.5	1101	9	CNS016LP	AL106903 Drosophil
c	19	99.8	8.4	684	8	AZ156639	AZ156639 SP_0023_B
	20	99.8	8.4	974	7	CK420551	AUF_IpTrk
c	21	99.8	8.4	1143	8	CC217764	CC217764 CH261-79O
c	22	99.6	8.4	960	5	BQ429353	BQ429353 AGENCOURT
c	23	99.4	8.4	631	5	BU292611	BU292611 603607414
	24	99.2	8.4	1107	6	CB905729	CB905729 tric075xn
	25	99.2	8.4	1107	7	CF877385	CF877385 tric075xn
	26	99.2	8.4	1246	9	CL058545	CL058545 CH216-88E
	27	99	8.4	523	8	AZ383375	AZ383375 1M0141E03
	28	98.8	8.4	537	9	CR080757	CR080757 Forward s
	29	98.8	8.4	1238	9	AG448606	AG448606 Mus muscu
c	30	98.8	8.4	1484	9	CL079800	CL079800 CH216-156
	31	98.6	8.3	432	9	BX998216	BX998216 Reverse s
	32	98.6	8.3	872	9	CNS02GHX	AL196350 Tetraodon
	33	98.6	8.3	1277	9	CG753585	CG753585 P048-3-H1
c	34	98.6	8.3	1471	9	CG748176	CG748176 P042-1-A0
	35	98.6	8.3	1555	9	CL073978	CL073978 CH216-131
c	36	98.4	8.3	1031	9	CL492176	CL492176 SAIL_564_
	37	98.4	8.3	1099	2	BF256465	BF256465 HVSMEf001
	38	98.4	8.3	1196	9	AG382042	AG382042 Mus muscu
	39	98.4	8.3	1546	9	AG435295	AG435295 Mus muscu
	40	98.4	8.3	1696	9	AG382169	AG382169 Mus muscu
	41	98.2	8.3	487	9	CNS0060P	AL062040 Drosophil
	42	98.2	8.3	567	8	AZ895651	AZ895651 RPCI-24-2
	43	98.2	8.3	883	8	AZ186646	AZ186646 SP_1007_B
	44	98.2	8.3	904	9	AG424774	AG424774 Mus muscu
	45	98.2	8.3	1106	6	CB905422	CB905422 tric074xf

ALIGNMENTS

RESULT 1
AG561854/c
LOCUS AG561854 776 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-481H05.T7, genomic survey sequence.
ACCESSION AG561854
VERSION AG561854.1 GI:48322552
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 776)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .776
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-481H05.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 666.8 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-25
Perfect score: 1182
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1020.8	86.4	9410	2	AAX20603	Aax20603 Polynucle
	2	777	65.7	2945	4	AAC84647	Aac84647 T. pallid
	3	721.4	61.0	939	4	AAC84649	Aac84649 T. pallid
	4	601.4	50.9	699	4	AAC84648	Aac84648 T. pallid
	5	110.8	9.4	628	12	ACH89664	Ach89664 Human gen
	6	108.2	9.2	795	2	AAV55830	Aav55830 FLGA inse
c	7	106	9.0	30191	12	ADQ97654	Adq97654 Mouse can
	8	105.8	9.0	799	2	AAV55831	Aav55831 Nucleotid
	9	105.8	9.0	1926	3	AAA50254	Aaa50254 Epstein B
	10	105.8	9.0	1926	4	AAF82902	Aaf82902 EBV tethe
	11	105.8	9.0	1926	10	ADK65580	Adk65580 Human her
	12	105.8	9.0	2580	3	AAA75454	Aaa75454 Nucleotid
	13	105.8	9.0	2580	6	AAI64275	Aai64275 Epstein-B
c	14	105.8	9.0	5452	2	AAX90923	Aax90923 Anti-sens
c	15	105.8	9.0	8705	2	AAZ23778	Aaz23778 Vector pS
c	16	105.8	9.0	8705	12	ADM10659	Adm10659 Expressio
c	17	105.8	9.0	9482	12	ADP64415	Adp64415 Vector pC
	18	105.8	9.0	9600	2	AAV21683	Aav21683 Vector pl
c	19	105.8	9.0	10285	6	ABS71027	Abs71027 pCEP-Xa-F
c	20	105.8	9.0	10285	6	ABS66453	Abs66453 Plasmid p
c	21	105.8	9.0	10330	12	ADL67154	Adl67154 Plasmid p
	22	105.8	9.0	10380	2	AAZ22248	Aaz22248 Nucleotid
c	23	105.8	9.0	10477	12	ADL67152	Adl67152 Plasmid p
c	24	105.8	9.0	10516	12	ADL67150	Adl67150 Plasmid p
c	25	105.8	9.0	10561	12	ADL67148	Adl67148 Plasmid p
	26	105.8	9.0	10596	2	AAQ51731	Aaq51731 Plasmid p
	27	105.8	9.0	10596	2	AAX15650	Aax15650 Nucleotid
	28	105.8	9.0	10596	2	AAT40348	Aat40348 Plasmid p
c	29	105.8	9.0	10615	12	ADL67175	Adl67175 Plasmid p
c	30	105.8	9.0	10774	12	ADL67153	Adl67153 Plasmid p
c	31	105.8	9.0	10921	12	ADL67151	Adl67151 Plasmid p
c	32	105.8	9.0	10961	12	ADL67149	Adl67149 Plasmid p
c	33	105.8	9.0	11006	12	ADL67147	Adl67147 Plasmid p
c	34	105.8	9.0	11059	12	ADL67176	Adl67176 Plasmid p
c	35	105.8	9.0	11693	13	ADR12379	Adr12379 Vector pC
	36	105.8	9.0	11924	12	ADO07395	Ado07395 Modified
	37	105.8	9.0	12242	12	ADO07394	Ado07394 Modified
c	38	105.8	9.0	16080	3	AAA59553	Aaa59553 DNA clone
c	39	105.8	9.0	17753	12	ADL71910	Adl71910 Expressio
	40	105.8	9.0	172281	12	ADN12161	Adn12161 Epstein-B
	41	105	8.9	8298	4	AAK72613	Aak72613 Human imm
	42	104.2	8.8	1925	2	AAX90924	Aax90924 Epstein B
c	43	100.8	8.5	26214	12	ADQ97246	Adq97246 Mouse can
	44	97.8	8.3	12733	6	ABK98631	Abk98631 Vector pE
	45	97.8	8.3	12733	9	ACD13882	Acd13882 L. lactis

ALIGNMENTS

RESULT 1
AAX20603
ID AAX20603 standard; DNA; 9410 BP.
XX
AC AAX20603;
XX
DT 05-MAY-1999 (first entry)
XX
DE Polynucleotide sequence from the genome of Treponema pallidum.
XX
KW Treponema pallidum infection; syphilis; Borrelia infection; animal;
KW enzyme production; ds.
XX
OS Treponema pallidum.
XX
PN WO9859034-A2.
XX
PD 30-DEC-1998.
XX
PF 23-JUN-1998; 98WO-US013041.
XX
PR 24-JUN-1997; 97US-0050667P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fraser CM;
XX
DR WPI; 1999-081273/07.
XX
PT New isolated Treponema pallidum nucleic acids - used to develop products
PT for the detection, diagnosis, characterisation, prevention and therapy of
PT T. pallidum infections, particularly syphilis.
XX
PS Claim 1; Page 693-698; 1150pp; English.
XX
CC AAX20500-21243 represent polynucleotide sequences from the genome of
CC Treponema pallidum. The sequences can be used for detection, diagnosis,
CC characterisation, prevention and therapy for T. pallidum infections,
CC particularly syphilis. They can also be used for detecting diseases
CC related to Borrelia infections in animals, and for the production of
CC biosynthetic products such as enzymes
XX
SQ Sequence 9410 BP; 1934 A; 2470 C; 2830 G; 2153 T; 0 U; 23 Other;

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 5749.51 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-23
Perfect score: 1287
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1287	100.0	1287	1	AF342807	AF342807 Treponema
	2	1125	87.4	14268	1	AE001220	AE001220 Treponema
	3	1067	82.9	1182	1	AF411126	AF411126 Treponema
	4	933.4	72.5	939	6	AX068036	AX068036 Sequence
	5	909	70.6	1647	1	AF411124	AF411124 Treponema
	6	896.4	69.7	2945	6	AX068032	AX068032 Sequence
	7	896.4	69.7	2946	1	AF015824	AF015824 Treponema
	8	797	61.9	1047	1	AF342806	AF342806 Treponema
	9	626.4	48.7	699	6	AX068034	AX068034 Sequence
	10	169.4	13.2	211580	2	AC111089	AC111089 Mus muscu
c	11	163	12.7	178757	10	AC122509	AC122509 Mus muscu
	12	154.4	12.0	197411	10	AC135961	AC135961 Mus muscu
c	13	154	12.0	260625	2	AC096018	AC096018 Rattus no
c	14	150.2	11.7	318930	2	AC073495	AC073495 Mus muscu
c	15	149.6	11.6	216602	10	AC136729	AC136729 Mus muscu
c	16	148.6	11.5	163945	2	AC116727	AC116727 Mus muscu
c	17	148.6	11.5	217353	10	AC149611	AC149611 Mus muscu
	18	148.6	11.5	229190	10	AC127348	AC127348 Mus muscu
	19	148	11.5	165592	10	AC122020	AC122020 Mus muscu
	20	147.8	11.5	211161	2	AC098271	AC098271 Rattus no
	21	147.6	11.5	152618	10	AC127583	AC127583 Mus muscu
	22	145.8	11.3	124244	10	AL929026	AL929026 Mouse DNA
	23	145.8	11.3	197683	10	AC118476	AC118476 Mus muscu
c	24	145.4	11.3	200574	10	BX005304	BX005304 Mouse DNA
	25	145.4	11.3	215745	10	AC117585	AC117585 Mus muscu
c	26	145.4	11.3	237814	10	AC091464	AC091464 Mus muscu
c	27	145	11.3	179206	2	AC124108	AC124108 Mus muscu
c	28	144.8	11.3	144093	10	AC109193	AC109193 Mus muscu
	29	144.6	11.2	110000	2	AC120236_0	AC120236 Rattus no
	30	144.6	11.2	192371	10	AC123857	AC123857 Mus muscu
c	31	144.2	11.2	120487	10	AC103637	AC103637 Mus muscu
c	32	144.2	11.2	171593	10	AC122052	AC122052 Mus muscu
c	33	144.2	11.2	203490	10	AC122851	AC122851 Mus muscu
c	34	143.8	11.2	182272	10	AC122232	AC122232 Mus muscu
c	35	143.8	11.2	191753	10	AC125235	AC125235 Mus muscu
c	36	143.2	11.1	194736	10	AC126271	AC126271 Mus muscu
	37	143.2	11.1	205054	10	AC098712	AC098712 Mus muscu
c	38	143	11.1	206497	10	AC084389	AC084389 Mus muscu
	39	142.8	11.1	152435	10	AC121566	AC121566 Mus muscu
	40	142.8	11.1	253504	10	AC102602	AC102602 Mus muscu
	41	142.6	11.1	125681	10	AC122889	AC122889 Mus muscu
	42	142.6	11.1	199459	10	AC125192	AC125192 Mus muscu
	43	142.2	11.0	178620	10	AC121865	AC121865 Mus muscu
	44	142.2	11.0	199854	10	AL591208	AL591208 Mouse DNA
c	45	142.2	11.0	208880	10	AC123837	AC123837 Mus muscu

ALIGNMENTS

RESULT 1
AF342807
LOCUS AF342807 1287 bp DNA linear BCT 13-SEP-2001
DEFINITION Treponema pallidum subsp. endemicum strain Bosnia acidic repeat protein (arp) gene, complete cds.
ACCESSION AF342807
VERSION AF342807.2 GI:15617206
KEYWORDS .
SOURCE Treponema pallidum subsp. endemicum
ORGANISM Treponema pallidum subsp. endemicum
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE 1 (bases 1 to 1287)
AUTHORS Liu,H. and Steiner,B.
TITLE Acidic repeat protein (arp) gene sequence of Treponema pallidum subspecies endemicum (Bosnia strain)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1287)
AUTHORS Liu,H., Steiner,B.M. and Rodes,B.
TITLE Molecular characterization of the acidic repeat protein (arp) of Treponema pallidum
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1287)
AUTHORS Liu,H. and Steiner,B.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2001) National Center for Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Rd. Mail Stop D13, Atlanta, GA 30333, USA
REFERENCE 4 (bases 1 to 1287)
AUTHORS Liu,H., Steiner,B. and Rodes,B.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2001) National Center for Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Rd. Mail Stop D13, Atlanta, GA 30333, USA
REMARK Sequence update by submitter
COMMENT On Sep 13, 2001 this sequence version replaced gi:12667500.
FEATURES Location/Qualifiers
source 1. .1287
/organism="Treponema pallidum subsp. endemicum"
/mol_type="genomic DNA"
/strain="Bosnia"
/sub_species="endemicum"
/db_xref="taxon:53436"

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:14 ; Search time 4570.53 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-23
Perfect score: 1287
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	134.8	10.5	776	9	AG561854	AG561854 Mus muscu
c	2	129	10.0	709	9	AG351718	AG351718 Mus muscu
c	3	126.2	9.8	650	8	AZ337339	AZ337339 1M0068B03
c	4	124.6	9.7	1089	4	BM468944	BM468944 AGENCOURT
	5	122.8	9.5	623	9	CR055317	CR055317 Reverse s
	6	122.8	9.5	1110	9	CL079755	CL079755 CH216-156
	7	122.8	9.5	1313	7	CF874294	CF874294 tric006xm
	8	122.6	9.5	523	8	AZ383375	AZ383375 1M0141E03
c	9	122	9.5	1945	8	CC251395	CC251395 CH261-157
	10	121.2	9.4	1083	7	CV520573	CV520573 0089P0047
	11	121.2	9.4	1448	8	CC220110	CC220110 CH261-92F
	12	120.4	9.4	860	6	CB904993	CB904993 tric040xp
c	13	120.2	9.3	697	6	BY752869	BY752869 BY752869
c	14	120.2	9.3	1031	9	CL492176	CL492176 SAIL_564_
c	15	120.2	9.3	1231	9	AG363910	AG363910 Mus muscu
	16	120	9.3	1555	9	CL073978	CL073978 CH216-131
	17	119.8	9.3	1560	9	CL081488	CL081488 CH216-162
c	18	119.8	9.3	1656	9	AG430456	AG430456 Mus muscu
	19	119.6	9.3	602	9	CR023579	CR023579 Reverse s
c	20	119.6	9.3	870	2	BE258873	BE258873 601116824
c	21	119.6	9.3	1292	8	CC208790	CC208790 CH261-26P
c	22	119.6	9.3	1484	9	CL079800	CL079800 CH216-156
	23	119.2	9.3	817	8	AZ196702	AZ196702 SP_1032_B
	24	119.2	9.3	1546	9	AG435295	AG435295 Mus muscu
	25	119	9.2	935	4	BI958090	BI958090 HVSMEn001
c	26	119	9.2	1153	8	CC294165	CC294165 CH261-130
c	27	118.8	9.2	517	9	TA21B11Q	AL453768 T. brucei
c	28	118.8	9.2	1100	8	CC262597	CC262597 CH261-167
	29	118.8	9.2	1233	9	AG396109	AG396109 Mus muscu
c	30	118.6	9.2	1196	8	CC298943	CC298943 CH261-22C
c	31	118.4	9.2	1035	9	CL086207	CL086207 ISB1-7A17
	32	118.4	9.2	1082	8	CC300639	CC300639 CH261-68J
c	33	118.4	9.2	1309	9	CL080508	CL080508 CH216-158
c	34	118.4	9.2	1373	9	AG435617	AG435617 Mus muscu
c	35	118.2	9.2	548	9	BX121682	BX121682 Danio rer
	36	118.2	9.2	837	9	CR074624	CR074624 Forward s
	37	118.2	9.2	883	8	AZ186646	AZ186646 SP_1007_B
	38	118.2	9.2	911	9	CR116264	CR116264 Forward s
	39	118.2	9.2	1238	9	AG448606	AG448606 Mus muscu
c	40	118.2	9.2	1471	9	CG748176	CG748176 P042-1-A0
	41	118.2	9.2	1696	9	AG382169	AG382169 Mus muscu
c	42	118	9.2	845	9	CC578225	CC578225 CH240_457
	43	118	9.2	1011	6	CB905602	CB905602 tric075xf
	44	118	9.2	1011	7	CF877292	CF877292 tric075xf
	45	118	9.2	1193	9	AG349830	AG349830 Mus muscu

ALIGNMENTS

RESULT 1
AG561854/c
LOCUS AG561854 776 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-481H05.T7, genomic survey sequence.
ACCESSION AG561854
VERSION AG561854.1 GI:48322552
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 776)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .776
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-481H05.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 726.034 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-23
Perfect score: 1287
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query % Match	Length	DB	ID	Description
	1	933.4	72.5	939	4	AAC84649	Aac84649 T. pallid
	2	933	72.5	9410	2	AAX20603	Aax20603 Polynucle
	3	896.4	69.7	2945	4	AAC84647	Aac84647 T. pallid
	4	626.4	48.7	699	4	AAC84648	Aac84648 T. pallid
c	5	130	10.1	30191	12	ADQ97654	Adq97654 Mouse can
	6	129.4	10.1	799	2	AAV55831	Aav55831 Nucleotid
	7	129.4	10.1	1926	3	AAA50254	Aaa50254 Epstein B
	8	129.4	10.1	1926	4	AAF82902	Aaf82902 EBV tethe
	9	129.4	10.1	1926	10	ADK65580	Adk65580 Human her
	10	129.4	10.1	2580	3	AAA75454	Aaa75454 Nucleotid
	11	129.4	10.1	2580	6	AAI64275	Aai64275 Epstein-B
c	12	129.4	10.1	5452	2	AAX90923	Aax90923 Anti-sens
c	13	129.4	10.1	8705	2	AAZ23778	Aaz23778 Vector pS
c	14	129.4	10.1	8705	12	ADM10659	Adm10659 Expressio
c	15	129.4	10.1	9482	12	ADP64415	Adp64415 Vector pC
	16	129.4	10.1	9600	2	AAV21683	Aav21683 Vector pl
c	17	129.4	10.1	10285	6	ABS71027	Abs71027 pCEP-Xa-F
c	18	129.4	10.1	10285	6	ABS66453	Abs66453 Plasmid p
c	19	129.4	10.1	10330	12	ADL67154	Adl67154 Plasmid p
	20	129.4	10.1	10380	2	AAZ22248	Aaz22248 Nucleotid
c	21	129.4	10.1	10477	12	ADL67152	Adl67152 Plasmid p
c	22	129.4	10.1	10516	12	ADL67150	Adl67150 Plasmid p
c	23	129.4	10.1	10561	12	ADL67148	Adl67148 Plasmid p
	24	129.4	10.1	10596	2	AAQ51731	Aaq51731 Plasmid p
	25	129.4	10.1	10596	2	AAX15650	Aax15650 Nucleotid
	26	129.4	10.1	10596	2	AAT40348	Aat40348 Plasmid p
c	27	129.4	10.1	10615	12	ADL67175	Adl67175 Plasmid p
c	28	129.4	10.1	10774	12	ADL67153	Adl67153 Plasmid p
c	29	129.4	10.1	10921	12	ADL67151	Adl67151 Plasmid p
c	30	129.4	10.1	10961	12	ADL67149	Adl67149 Plasmid p
c	31	129.4	10.1	11006	12	ADL67147	Adl67147 Plasmid p
c	32	129.4	10.1	11059	12	ADL67176	Adl67176 Plasmid p
c	33	129.4	10.1	11693	13	ADR12379	Adr12379 Vector pC
	34	129.4	10.1	11924	12	ADO07395	Ado07395 Modified
	35	129.4	10.1	12242	12	ADO07394	Ado07394 Modified
c	36	129.4	10.1	16080	3	AAA59553	Aaa59553 DNA clone
c	37	129.4	10.1	17753	12	ADL71910	Adl71910 Expressio
	38	129.4	10.1	172281	12	ADN12161	Adn12161 Epstein-B
	39	129.2	10.0	1925	2	AAX90924	Aax90924 Epstein B
	40	128.4	10.0	795	2	AAV55830	Aav55830 FLGA inse
	41	125.2	9.7	628	12	ACH89664	Ach89664 Human gen
c	42	120.8	9.4	26214	12	ADQ97246	Adq97246 Mouse can
	43	118.8	9.2	12733	6	ABK98631	Abk98631 Vector pE
	44	118.8	9.2	12733	9	ACD13882	Acd13882 L. lactis
	45	118.8	9.2	12739	6	ABK98592	Abk98592 Vector pE

ALIGNMENTS

RESULT 1
AAC84649
ID AAC84649 standard; DNA; 939 BP.
XX
AC AAC84649;
XX
DT 11-SEP-2003 (revised)
DT 20-APR-2001 (first entry)
XX
DE T. pallidum (Bosnia) acidic repeat protein (arp) encoding DNA.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel; ds.
XX
OS Treponema pallidum; ssp. endemicum.
XX
FH Key Location/Qualifiers
FT CDS 1. .939
FT /*tag= a
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
DR P-PSDB; AAB48318.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 19; Fig 9; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 4677.34 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-21
Perfect score: 1047
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1047

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1047	100.0	1047	1	AF342806	AF342806 Treponema
	2	902	86.2	1182	1	AF411126	AF411126 Treponema
	3	847.6	81.0	14268	1	AE001220	AE001220 Treponema
	4	797	76.1	1287	1	AF342807	AF342807 Treponema
	5	693.4	66.2	699	6	AX068034	AX068034 Sequence
	6	653	62.4	1647	1	AF411124	AF411124 Treponema
	7	642	61.3	2945	6	AX068032	AX068032 Sequence
	8	642	61.3	2946	1	AF015824	AF015824 Treponema
	9	626.4	59.8	939	6	AX068036	AX068036 Sequence
	10	89.4	8.5	211580	2	AC111089	AC111089 Mus muscu
	11	88.4	8.4	165592	10	AC122020	AC122020 Mus muscu
	12	87.8	8.4	219771	2	BX005376	BX005376 Danio rer
	13	87.8	8.4	253504	10	AC102602	AC102602 Mus muscu
	14	87.8	8.4	266556	2	AC136868	AC136868 Rattus no
c	15	87.6	8.4	233939	2	AC105853	AC105853 Rattus no
	16	87.2	8.3	269572	2	AC108552	AC108552 Rattus no
c	17	86.8	8.3	110000	10	AE016753_2	Continuation (3 of
	18	86.8	8.3	152435	10	AC121566	AC121566 Mus muscu
	19	86.2	8.2	125681	10	AC122889	AC122889 Mus muscu
c	20	86.2	8.2	161905	10	AL929034	AL929034 Mouse DNA
c	21	86.2	8.2	178757	10	AC122509	AC122509 Mus muscu
	22	86.2	8.2	196236	10	AC108780	AC108780 Mus muscu
	23	86.2	8.2	197411	10	AC135961	AC135961 Mus muscu
c	24	86.2	8.2	203086	10	AC099948	AC099948 Mus muscu
c	25	86.2	8.2	215769	10	AC100209	AC100209 Mus muscu
	26	85.6	8.2	192371	10	AC123857	AC123857 Mus muscu
	27	85.6	8.2	199459	10	AC125192	AC125192 Mus muscu
	28	85.2	8.1	143913	2	AC124827	AC124827 Mus muscu
c	29	84.6	8.1	120487	10	AC103637	AC103637 Mus muscu
c	30	84.6	8.1	163882	10	AC133904	AC133904 Mus muscu
c	31	84.6	8.1	171593	10	AC122052	AC122052 Mus muscu
	32	84.6	8.1	179063	10	AC145590	AC145590 Mus muscu
c	33	84.6	8.1	191753	10	AC125235	AC125235 Mus muscu
c	34	84.6	8.1	199854	10	AL591208	AL591208 Mouse DNA
c	35	84.6	8.1	210595	2	AC116862	AC116862 Mus muscu
c	36	84.6	8.1	215620	10	AL928551	AL928551 Mouse DNA
c	37	84.6	8.1	217353	10	AC149611	AC149611 Mus muscu
	38	84.6	8.1	229190	10	AC127348	AC127348 Mus muscu
c	39	84.6	8.1	234888	2	AC102097	AC102097 Mus muscu
c	40	84.6	8.1	260625	2	AC096018	AC096018 Rattus no
	41	84.6	8.1	289751	10	AC091458	AC091458 Mus muscu
	42	84	8.0	179886	2	AC140072	AC140072 Mus muscu
c	43	84	8.0	182272	10	AC122232	AC122232 Mus muscu
c	44	84	8.0	208880	10	AC123837	AC123837 Mus muscu
c	45	84	8.0	219568	10	AL844840	AL844840 Mouse DNA

ALIGNMENTS

RESULT 1
AF342806
LOCUS AF342806 1047 bp DNA linear BCT 13-SEP-2001
DEFINITION Treponema pallidum subsp. pertenue strain CDC2 acidic repeat protein (arp) gene, complete cds.
ACCESSION AF342806
VERSION AF342806.2 GI:15617204
KEYWORDS .
SOURCE Treponema pallidum subsp. pertenue (yaws treponeme)
ORGANISM Treponema pallidum subsp. pertenue
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Liu,H. and Steiner,B.
TITLE Acidic repeat protein (arp) gene sequence of Treponema pallidum subspecies pertenue (CDC 2 strain)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Liu,H., Steiner,B.M. and Rodes,B.
TITLE Molecular characterization of the acidic repeat protein (arp) of Treponema pallidum
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1047)
AUTHORS Liu,H. and Steiner,B.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2001) National Center for Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Rd. Mail Stop D13, Atlanta, GA 30333, USA
REFERENCE 4 (bases 1 to 1047)
AUTHORS Liu,H., Steiner,B. and Rodes,B.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2001) National Center for Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Rd. Mail Stop D13, Atlanta, GA 30333, USA
REMARK Sequence update by submitter
COMMENT On Sep 13, 2001 this sequence version replaced gi:12667498.
FEATURES Location/Qualifiers
source 1. .1047
/organism="Treponema pallidum subsp. pertenue"
/mol_type="genomic DNA"
/strain="CDC2"
/sub_species="pertenue"
/db_xref="taxon:168"

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:14 ; Search time 3718.21 Seconds
(without alignments)
10718.395 Million cell updates/sec

Title: US-10-017-168-21
Perfect score: 1047
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1047

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	89.6	8.6	365	9	L2644X	AL160994 Leishmani
c	2	85.8	8.2	293	8	AZ334000	AZ334000 1M0063P17
c	3	83	7.9	776	9	AG561854	AG561854 Mus muscu
c	4	81.4	7.8	709	9	AG351718	AG351718 Mus muscu
c	5	77	7.4	697	6	BY752869	BY752869 BY752869
c	6	76.6	7.3	514	8	BZ089457	BZ089457 CH230-1C1
c	7	76.6	7.3	783	9	AG573654	AG573654 Mus muscu
c	8	75.4	7.2	820	9	CL836578	OR_CBa006
	9	73.4	7.0	482	7	CV254879	CV254879 WS02411.B
	10	73.2	7.0	752	9	AG562801	AG562801 Mus muscu
c	11	72.8	7.0	650	8	AZ337339	AZ337339 1M0068B03
	12	72.2	6.9	384	9	CNS01145	AL099791 Drosophil
	13	71.8	6.9	523	8	AZ383375	AZ383375 1M0141E03
c	14	71.8	6.9	979	6	CD328191	AGENCOURT
	15	71.4	6.8	419	4	BG273097	BG273097 nai99f06.
c	16	70.8	6.8	1945	8	CC251395	CC251395 CH261-157
c	17	70.6	6.7	275	7	CO546011	LyEST2038
c	18	70.4	6.7	733	9	CC641774	OGUBU35TH
c	19	70.4	6.7	852	8	BZ801844	PUGAG07TB
c	20	70.4	6.7	945	9	CG344918	OG2BH42TH
c	21	70.4	6.7	1099	9	CL509275	CL509275 SAIL_811_
	22	70.2	6.7	617	9	CE019059	CE019059 tigr-gss-
	23	70.2	6.7	696	7	CK138139	VRJ135 Vi
c	24	70	6.7	834	9	AG555306	AG555306 Mus muscu
c	25	70	6.7	1197	9	AG346705	AG346705 Mus muscu
c	26	69.4	6.6	427	7	CK286024	CK286024 EST748746
c	27	69.4	6.6	1147	8	BZ051981	BZ051981 jnr56f09.
	28	69.2	6.6	699	6	CD493768	CD493768 CDA07-A05
c	29	69.2	6.6	1271	9	CL492192	CL492192 SAIL_564_
	30	69	6.6	430	5	BM900946	BM900946 rc43c10.y
	31	69	6.6	986	9	AG390365	AG390365 Mus muscu
c	32	68.6	6.6	494	7	CF609053	CF609053 GERMO01_0
c	33	68.6	6.6	516	7	CF607575	CF607575 GEMMA01_0
	34	68.6	6.6	583	5	BQ847872	BQ847872 QGA5J16.y
c	35	68.6	6.6	1344	9	AG435591	AG435591 Mus muscu
c	36	68.4	6.5	501	7	CV094178	CV094178 FAMU_USDA
c	37	68.4	6.5	520	7	CV096855	CV096855 FAMU_USDA
c	38	68.4	6.5	552	7	CN605345	CN605345 USDA_FP_1
c	39	68.4	6.5	592	7	CV092833	CV092833 FAMU_USDA
c	40	68.4	6.5	609	7	CV099895	CV099895 FAMU_USDA
c	41	68.4	6.5	624	7	CV092434	CV092434 FAMU_USDA
c	42	68.4	6.5	647	7	CV096641	CV096641 FAMU_USDA
c	43	68.4	6.5	651	7	CV093263	CV093263 FAMU_USDA
c	44	68.4	6.5	651	7	CV097413	CV097413 FAMU_USDA
c	45	68.4	6.5	688	7	CV098193	CV098193 FAMU_USDA

ALIGNMENTS

RESULT 1
L2644X/c
LOCUS L2644X 365 bp DNA linear GSS 16-MAR-2000
DEFINITION Leishmania major Friedlin cosmid L2644 t3Hyg end-sequence, similar to U40394 U40394 Kaposi's sarcoma-associated herpes-like. . ., N=755, Prob=1.8e-54; TR:P93797 P93797 PHEROPHORIN-S PRECURSOR. [0] +3. . ., N=318, Prob=7.2e-37, genomic survey sequence.
ACCESSION AL160994
VERSION AL160994.1 GI:7258621
KEYWORDS GSS.
SOURCE Leishmania major
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
REFERENCE 1 (bases 1 to 365)
AUTHORS Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.
TITLE A physical map of the Leishmania major Friedlin genome
JOURNAL Genome Res. 8 (2), 135-145 (1998)
MEDLINE 98146435
PUBMED 9477341
REFERENCE 2 (bases 1 to 67)
AUTHORS Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk
COMMENT see http://www.ebi.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/
The cLHYG t3Hyg primer sequence can be obtained from acc. no. U59231.
FEATURES Location/Qualifiers
source 1. .365
/organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/chromosome="26"
/clone="cosmid L2644"
ORIGIN

Query Match 8.6%; Score 89.6; DB 9; Length 365;
Best Local Similarity 58.7%; Pred. No. 1.5e-13;
Matches 155; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 590.643 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-21
Perfect score: 1047
Sequence: 1 atgtttgtgcgcagtgacat.....ttctgaaaaaggcgcgatga 1047

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		852.2	81.4	9410	2	AAX20603	Aax20603 Polynucle
2		693.4	66.2	699	4	AAC84648	Aac84648 T. pallid
3		642	61.3	2945	4	AAC84647	Aac84647 T. pallid
4		626.4	59.8	939	4	AAC84649	Aac84649 T. pallid
5		82.6	7.9	149158	12	ADP74211	Adp74211 Equine he
6	c	82.6	7.9	149158	12	ADP74211	Adp74211 Equine he
7		82.6	7.9	149261	12	ADP74212	Adp74212 Equine he
8	c	82.6	7.9	149261	12	ADP74212	Adp74212 Equine he
9		82.6	7.9	150071	12	ADP74216	Adp74216 Equine he
10	c	82.6	7.9	150071	12	ADP74216	Adp74216 Equine he
11		82.6	7.9	150223	12	ADP74201	Adp74201 Equine he
12	c	82.6	7.9	150223	12	ADP74201	Adp74201 Equine he
13	c	80.6	7.7	110000	8	ABX16390_2	Continuation (3 of
14		78.2	7.5	628	12	ACH89664	Ach89664 Human gen
15		78.2	7.5	3012	12	ADN12155	Adn12155 Herpesvir
16		77.6	7.4	3127	12	ADN12154	Adn12154 Kaposis s
17	c	77.4	7.4	114793	4	AAD08215	Aad08215 Human gen
18	c	75.8	7.2	7720	3	AAA53800	Aaa53800 Genomic D
19		75.8	7.2	8298	4	AAK72613	Aak72613 Human imm
20	c	75	7.2	16442	2	AAX83006	Aax83006 Partial m
21		73.4	7.0	795	2	AAV55830	Aav55830 FLGA inse
22		73.4	7.0	799	2	AAV55831	Aav55831 Nucleotid
23		73.4	7.0	1925	2	AAX90924	Aax90924 Epstein B
24		73.4	7.0	1926	3	AAA50254	Aaa50254 Epstein B
25		73.4	7.0	1926	4	AAF82902	Aaf82902 EBV tethe
26		73.4	7.0	1926	10	ADK65580	Adk65580 Human her
27		73.4	7.0	2580	3	AAA75454	Aaa75454 Nucleotid
28		73.4	7.0	2580	6	AAI64275	Aai64275 Epstein-B
29	c	73.4	7.0	5452	2	AAX90923	Aax90923 Anti-sens
30	c	73.4	7.0	8705	2	AAZ23778	Aaz23778 Vector pS
31	c	73.4	7.0	8705	12	ADM10659	Adm10659 Expressio
32	c	73.4	7.0	9482	12	ADP64415	Adp64415 Vector pC
33		73.4	7.0	9600	2	AAV21683	Aav21683 Vector pl
34	c	73.4	7.0	10285	6	ABS71027	Abs71027 pCEP-Xa-F
35	c	73.4	7.0	10285	6	ABS66453	Abs66453 Plasmid p
36	c	73.4	7.0	10330	12	ADL67154	Adl67154 Plasmid p
37		73.4	7.0	10380	2	AAZ22248	Aaz22248 Nucleotid
38	c	73.4	7.0	10477	12	ADL67152	Adl67152 Plasmid p
39	c	73.4	7.0	10516	12	ADL67150	Adl67150 Plasmid p
40	c	73.4	7.0	10561	12	ADL67148	Adl67148 Plasmid p
41		73.4	7.0	10596	2	AAQ51731	Aaq51731 Plasmid p
42		73.4	7.0	10596	2	AAX15650	Aax15650 Nucleotid
43		73.4	7.0	10596	2	AAT40348	Aat40348 Plasmid p
44	c	73.4	7.0	10615	12	ADL67175	Adl67175 Plasmid p
45	c	73.4	7.0	10774	12	ADL67153	Adl67153 Plasmid p

ALIGNMENTS

RESULT 1
AAX20603
ID AAX20603 standard; DNA; 9410 BP.
XX
AC AAX20603;
XX
DT 05-MAY-1999 (first entry)
XX
DE Polynucleotide sequence from the genome of Treponema pallidum.
XX
KW Treponema pallidum infection; syphilis; Borrelia infection; animal;
KW enzyme production; ds.
XX
OS Treponema pallidum.
XX
PN WO9859034-A2.
XX
PD 30-DEC-1998.
XX
PF 23-JUN-1998; 98WO-US013041.
XX
PR 24-JUN-1997; 97US-0050667P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fraser CM;
XX
DR WPI; 1999-081273/07.
XX
PT New isolated Treponema pallidum nucleic acids - used to develop products
PT for the detection, diagnosis, characterisation, prevention and therapy of
PT T. pallidum infections, particularly syphilis.
XX
PS Claim 1; Page 693-698; 1150pp; English.
XX
CC AAX20500-21243 represent polynucleotide sequences from the genome of
CC Treponema pallidum. The sequences can be used for detection, diagnosis,
CC characterisation, prevention and therapy for T. pallidum infections,
CC particularly syphilis. They can also be used for detecting diseases
CC related to Borrelia infections in animals, and for the production of
CC biosynthetic products such as enzymes
XX
SQ Sequence 9410 BP; 1934 A; 2470 C; 2830 G; 2153 T; 0 U; 23 Other;